This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Scott, Matthew P.
Goodrich, Lisa V.
Johnson, Ronald L.

(ii) TITLE OF INVENTION: Mammalian Patched Gene and Its Use

(iii) NUMBER OF SEQUENCES: 20

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
(B) STREET: 4 Embarcadero Center, Suite 3400
(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94111-4187

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Rowland, Bertram I
(B) REGISTRATION NUMBER: 20,015
(C) REFERENCE/DOCKET NUMBER: A60190/BIR STAN171

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (415) 781-1989
(B) TELEFAX: (415) 398-3249
(C) TELEX: 910277299

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 680 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AACCTATGGC ACCCCCCCCA ACCTTTCCTA ACAAAACCCC TTTATACCCC CTTAAATTTT 60

CCACCCAAAC CCTGAACAGA AACCTTTTTA ACCCCCCCCA CCCGGAATTC CATCCCCCCC 120

AAATTACAAC TCCAGCCAAA ATTAAAATTG GTCCTAACCT AACCATGTTG TTACGGTTTC 180

CCCCCCCAAA TACATGCACT GGCCCGAACA CTTGATCGTT GCCGTTCCAA TAAGAATAAA 240

TCTGGTCATA TTAAACAAGC CAAAGCTTTA CAAACTGTTG TACAATTAAT GGGCGAACAC 300

GAACTGTTCG AATTCTGGTC TGGACATTAC AAAGTGCACC ACATCGGATG GAACCAGGAG 360

AAGGCCACAA CCGTACTGAA CGCCTGGCAG AAGAAGTTCG CACAGGTTGG TGGTTGGCGC 420

AAGGAGTAGA GTGAATGGTG GTAATTTTTG GTTGTTCCAG GAGGTGGATC GTCTGACGAA 480

GAGCAAGAAG TCGTCGAATT ACATCTTCGT GACGTTCTCC ACCGCCAATT TGAACAAGAT 540

GTTGAAGGAG GCGTCGAAAC GGACGTGGTG AAGCTGGGGG TGGTGCTGGG GGTGGCGGCG 600

GTGTACGGGT GGGTGGCCCA GTCGGGGCTG GCTGCCTTGG GAGTGCTGGT CTTGCGGCTC 660

ATTCGCCCTA TAGTAGCGTA 680

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa Pro Pro Pro Asn Tyr Asn Ser Xaa Pro Lys Xaa Xaa Xaa Leu Val
1 5 10 15

Leu Thr Pro Xaa Val Val Thr Val Ser Pro Pro Lys Tyr Met His Trp
20 25 30

Pro Glu His Leu Ile Val Ala Val Pro Ile Arg Ile Asn Leu Val Ile
35 40 45

Leu Asn Lys Pro Lys Ala Leu Gln Thr Val Val Gln Leu Met Gly Glu
50 55 60

His Glu Leu Phe Glu Phe Trp Ser Gly His Tyr Lys Val His His Ile
65 70 75 80

Gly Trp Asn Gln Glu Lys Ala Thr Thr Val Leu Asn Ala Trp Gln Lys
85 90 95

Lys Phe Ala Gln Val Gly Gly Trp Arg Lys Glu
100 105

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4448 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGCCAGTGTC GACACGCTGT TAAGGTGTTA CGAAACTATC GAAACTCTGT ACCGTTCCGT 60

GTTACATTCG GTCAGTGATA AACAGAAGTG AATAATTCGG GTGTACAAGT GTGTGGTTAT 120

GTGGCGGCGA GTGATATGAC AGCGTGCGCC GCCAGACGGA TTCCAGCCGT CTTCATGAGG 180

ATATCGGTGA CAAGCCTGGC CCCGAGATCA TGGTGGCTCC CGATTCCGAG GCTCCTTCGA 240

ATCCTCGGAT AACGGCTGCA CACGAGAGCC CCTGCGCCAC CGAGGCGCGC CACAGTGCTG 300

ATCTTTACAT ACGTACCAGT TGGGTGGACG CCGCACTAGC TCTCTCTGAA CTCGAAAAGG 360

GTAACATCGA AGGAGGAAGA ACCTCTCTGT GGATACGAGC GTGGCTACAA GAACAGCTCT 420

TTATTTTGGG CTGCTTTCTT CAAGGCGACG CGGGGAAAGT CCTCTTCGTT GCCATCCTCG 480

TTCTGTCGAC GTTCTGCGTC GGTCTCAAGT CAGCACAAAT ACATACAAGG GTCGACCAAC 540

TCTGGGTTCA AGAGGGTGGT AGATTAGAAG CCGAGTTGAA ATATACAGCG CAAGCTTTGG 600

GCGAGGCGGA CTCCTCGACG CACCAGCTTG TCATACAAAC TGCCAAAGAT CCAGACGTCT 660

CCCTGCTACA TCCAGGCGCG TTGCTTGAAC ACCTTAAGGT GGTGCACGCA GCGACTCGGG 720

153
154 TGACAGTTCA CATGTACGAC ATTGAGTGGC GCCTCAAAGA CCTGTGCTAC AGCCCCAGCA 780
155
156 TACCGGACTT CGAGGGTTAC CACCACATCG AGTCAATCAT AGACAACGTC ATCCCCTGCG 840
157
158 CTATTATCAC CCCCCTTGAT TGCTTCTGGG AAGGCTCCAA GTTGCTTGGT CCCGATTATC 900
159
160 CTATATACGT ACCACATCTT AAACACAAAC TACAATGGAC ACATTTAAAT CCATTGGAAG 960
161
162 TTGTAGAAGA AGTGAAAAAA TTAAAGTTCC AATTTCCTCT GAGCACAATA GAGGCGTACA 1020
163
164 TGAAGAGAGC CGGCATCACT TCCGCCTACA TGAAAAAGCC GTGCTTAGAC CCCACCGACC 1080
165
166 CACATTGTCC AGCCACGGCT CCAAACAAAA AGTCTGGTCA TATTCCAGAT GTAGCGGCGG 1140
167
168 AGCTGTCGCA CGGATGTTAT GGTTTCGCGG CAGCTTACAT GCACTGGCCG GAACAGTTAA 1200
169
170 TTGTAGGGGG AGCTACAAGG AATTCGACAT CAGCTCTGAG AAAAGCACGC GTTTACAGAC 1260
171
172 TGTAGTACAG TTAATGGGCG AGAGAGAAAT GTACGAGTAC TGGGCCGATC ATTATAAAGT 1320
173
174 ACATCAAATT GGCTGGAATC AAGAGAAGGC AGCTGCTGTA CTGGATGCCT GGCAGAGAAA 1380
175
176 GTTTGCCGCT GAAGTCAGAA AAATTACTAC CTCAGGATCA GTATCATCGG CTTATAGTTT 1440
177
178 CTATCCGTTC TCCACCTCGA CACTTAATGA CATACTCGGG AAGTTCTCCG AAGTGTCACT 1500
179
180 GAAGAACATT ATATTAGGCT ATATGTTTAT GTTAATTTAT GTTGCCGTTA CTTTAATACA 1560
181
182 ATGGCGGGAT CCGATTCGCT CGCAAGCGGG TGTGGGTATC GCCGGAGTTC TACTACTATC 1620
183
184 AATCACTGTT GCCGCTGGCT TAGGATTTTG TGCTTTATTA GGCATACCAT TCAACGCTTC 1680
185
186 AAGTACGCAA ATAGTACCAT TCCTAGCGCT CGGGTTAGGA GTTCAAGATA TGTTTCTTCT 1740
187
188 CACTCACACG TATGTGGAGC AAGCGGGAGA TGTGCCTAGA GAAGAGAGGA CTGGACTTGT 1800
189
190 ATTGAAAAAG AGCGGTTTAA GCGTACTTCT GGCGTCTTTG TGCAACGTGA TGGCATTTTT 1860
191
192 GGCAGCAGCC CTTCTACCTA TTCCAGCTTT CAGAGTATTT TGCCTACAGG CTGCCATACT 1920
193
194 TCTTCTGTTT AACTTGGGGT CAATATTACT GGTTTTTCCT GCTATGATCT CGTTAGACCT 1980
195
196 GCGACGGAGG TCAGCCGCGA GGGCCGATCT TTTATGCTGT TTGATGCCTG AGAGTCCATT 2040
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198 ACCGAAGAAG AAAATTCCGG AAAGAGCAAA AACTAGAAAA AACGATAAGA CTCATAGGAT 2100
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200 AGACACCACG AGACAACCTC TAGACCCAGA TGTGTCCGAG AACGTGACCA AAACTTGCTG 2160
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202 CTTAAGCGTC TCGCTCACCA AGTGGGCCAA GAACCAATAC GCGCCGTTCA TCATGCGCCC 2220
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204 CGCTGTTAAG GTTACATCCA TGTTAGCGTT GATTGCTGTT ATTCTGACTA GCGTTTGGGG 2280
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206 AGCGACAAAA GTAAAGGATG GATTGGATTT GACTGATATT GTACCGGAGA ATACAGACGA 2340
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208 ACACGAATTT TTATCTCGTC AGGAAAAATA CTTTGGCTTC TATAATATGT ACGCCGTGAC 2400
209
210 GCAAGGCAAC TTTGAATATC CCACCAATCA GAAGTTATTA TATGAGTATC ACGATCAATT 2460
211
212 CGTCAGAATA CCTAATATAA TCAAGAATGA TAACGGCGGT CTCACGAAAT TTTGGTTGAG 2520
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214 TTTATTCCGC GACTGGTTAT TGGACTTGCA AGTGGCTTTT GATAAGGAGG TTGCCAGCGG 2580
215
216 TTGTATAACA CAAGAGTATT GGTGCAAAAA CGCGAGTGAC GAAGGAATAT TGGCCTATAA 2640
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218 ACTTATGGTG CAGACTGGCC ATGTGGACAA TCCAATCGAT AAGTCTCTGA TTACGGCAGG 2700
219
220 TCACAGACTA GTTGACAAAG ACGGTATTAT AAATCCAAAG GCATTTTATA ATTACCTATC 2760
221
222 AGCTTGGGCT ACTAACGACG CGTTGGCATA CGGAGCCTCA CAAGGGAACT TGAAACCTCA 2820
223
224 GCCCCAAAGA TGGATCCATT CTCCGGAGGA TGTACATTTA GAAATAAAGA AATCGTCGCC 2880
225
226 ATTAATTTAC ACACAGTTAC CATTCTACCT TTCCGGTCTC AGCGACACTA TAGCATCAAA 2940
227
228 ACGTTGATAA GATCTGTGCG AGATTTATGT CTGAAGTACG AGGCGAAAGG TTTACCGAAC 3000
229
230 TTTCCATCGG GTATACCATT CCTTTTCTGG GAACAGTATT TGTATTTAAG GACATCTTTA 3060
231
232 CTACTGGCTT TGGCGTGTGC TTTGGCAGCT GTCTTCATTG CGGTTATGGT GCTATTGTTG 3120
233
234 AACGCCTGGG CAGCAGTACT GGTGACATTA GCGCTGGCTA CATTAGTACT GCAGCTGTTA 3180
235
236 GGTGTATGGC CTTATTGGGC GTGAAGCTAT CTGCAATGCC GGCCGTACTA CTGGTGCTAG 3240
237
238 CCATTGGGAG AGGAGTTCAC TTCACTGTGC ATTTATGTTT GGGTTTTGTA ACATCAATCG 3300
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240 GTTGCAAGCG GCGCCGCGCG TCACTAGCTC TAGAATCAGT TCTGGCGCCA GTGGTGCACG 3360
241
242 GCGCTCTGGC GGCCGCGCTG GCTGCCTCGA TGCTAGCTGC AAGTGAATGT GGCTTCGTTG 3420
243
244 CCAGACTGTT CTTGAGGTTA CTACTGGACA TCGTGTTTCT GGGACTCATC GATGGGTTGC 3480
245
246 TGTTCTTCCC TATTGTCCTT TCGATATTGG GACCGGCTGC TGAGGTACGA CCTATAGAGC 3540
247
248 ATCCAGAACG CTTATCGACT CCATCGCCAA AATGTTCGCC CATCCACCCT CGCAAATCAA 3600
249
250 GTTCCAGCTC AGGCGGTGGT GATAAATCAA GTCGAACCAG TAAATCAGCA CCAAGGCCTT 3660
251
252 GCGCACCATC TCTCACGACC ATTACTGAAG AGCCTTCGAG TTGGCACAGT TCCGCCCACT 3720
253
254 CCGTACAATC TTCTATGCAG TCGATAGTGG TCCAGCCGGA GGTGGTGGTC GAAACTACCA 3780
255
256 CGTATAATGG CAGCGATTCT GCTTCAGGAC GGTCGACGCC TACAAAGTCT TCACACGGTG 3840
257
258 GTGCTATCAC AACTACTAAG GTGACCGCCA CGGCAAATAT AAAGGTAGAA GTGGTGACAC 3900

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/319,745*

DATE: 10/24/94
TIME: 10:57:24

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